



OIKE

RAW SEQUENCE LISTING

DATE: 03/18/2002

PATENT APPLICATION: US/09/722,544A

TIME: 15:28:22

Input Set : A:\07334-362001.txt

Output Set: N:\CRF3\03182002\I722544A.raw

Does Not Comply
Corrected Diskette Needed

```

3 <110> APPLICANT: Hong, Chen
4   Freimer, Nelson B.
6 <120> TITLE OF INVENTION: METHODS OF DIAGNOSING NEUROPSYCHIATRIC DISORDERS
8 <130> FILE REFERENCE: 07334-362001
10 <140> CURRENT APPLICATION NUMBER: 09/722,544A
11 <141> CURRENT FILING DATE: 2000-11-28
13 <150> PRIOR APPLICATION NUMBER: 09/236,134
14 <151> PRIOR FILING DATE: 1999-01-22
16 <150> PRIOR APPLICATION NUMBER: 60/078,044
17 <151> PRIOR FILING DATE: 1998-03-16
19 <150> PRIOR APPLICATION NUMBER: 60/088,312
20 <151> PRIOR FILING DATE: 1998-06-05
22 <150> PRIOR APPLICATION NUMBER: 60/106,056
23 <151> PRIOR FILING DATE: 1998-10-28
25 <160> NUMBER OF SEQ ID NOS: 33
27 <170> SOFTWARE: FastSEQ for Windows Version 3.0

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ERRORED SEQUENCES

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246 <210> SEQ ID NO: 3
247 <211> LENGTH: 1957
248 <212> TYPE: DNA
249 <213> ORGANISM: Homo sapiens
251 <220> FEATURE:
252 <221> NAME/KEY: CDS
253 <222> LOCATION: (241)...(1671)
E--> 255 <400> SEQUENCE: ① 3
256 tgcgtcacct gcaggccccgg gccgcgggggt tggtttccac cctggagggtt gctgacaccc 60
257 tgtgccctcg gctgacttcc agccggtggc acagacgcct ccagggggca gcactcaagc 120
258 gcatcttagg aatgacagag ttgcgtccct ctckgttgcc aggctggagt tcagtggcat 180
259 gttcwttagct cactgaagcc tcaaattcct gggttcaagt gaccctccya cctcagcccc 240
260 atg agg acc tgg gac tac agt aac agc ggg aac atg aag ccg cca ctc 288
261 Met Arg Thr Trp Asp Tyr Ser Asn Ser Gly Asn Met Lys Pro Pro Leu
262 1 5 10 15
264 ttg gtg ttt att gtg tgt ctg ctg tgg ttg aaa gac agt cac tgc gca 336
265 Leu Val Phe Ile Val Cys Leu Leu Trp Leu Lys Asp Ser His Cys Ala
266 20 25 30
268 ccc act tgg aag gac aaa act gct atc agt gaa aac ctg aag agt ttt 384
269 Pro Thr Trp Lys Asp Lys Thr Ala Ile Ser Glu Asn Leu Lys Ser Phe
270 35 40 45
272 tct gag gtg ggg gag ata gat gca gat gaa gag gtg aag aag gct ttg 432
273 Ser Glu Val Gly Glu Ile Asp Ala Asp Glu Glu Val Lys Lys Ala Leu

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274	50	55	60	
276	act ggt att aag caa atg aaa atc atg atg gaa aga aaa gag aag gaa	480		
277	Thr Gly Ile Lys Gln Met Lys Ile Met Met Glu Arg Lys Glu Lys Glu			
278	65 70 75 80			
280	cac acc aat cta atg agc acc ctg aag aaa tgc aga gaa gaa aag cag	528		
281	His Thr Asn Leu Met Ser Thr Leu Lys Lys Cys Arg Glu Glu Lys Gln			
282	85 90 95			
284	gag gcc ctg aaa ctt ctg aat gaa gtt caa gaa cat ctg gag gaa gaa	576		
285	Glu Ala Leu Lys Leu Leu Asn Glu Val Gln Glu His Leu Glu Glu			
286	100 105 110			
288	gaa agg cta tgc cgg gag tct ttg gca gat tcc tgg ggt gaa tgc agg	624		
289	Glu Arg Leu Cys Arg Glu Ser Leu Ala Asp Ser Trp Gly Glu Cys Arg			
290	115 120 125			
292	tct tgc ctg gaa aat aac tgc atg aga att tat aca acc tgc caa cct	672		
293	Ser Cys Leu Glu Asn Asn Cys Met Arg Ile Tyr Thr Thr Cys Gln Pro			
294	130 135 140			
296	agc tgg tcc tct gtg aaa aat aag att gaa cgg ttt ttc agg aag ata	720		
297	Ser Trp Ser Ser Val Lys Asn Lys Ile Glu Arg Phe Phe Arg Lys Ile			
298	145 150 155 160			
300	tat caa ttt cta ttt cct ttc cat gaa gat aat gaa aaa gat ctc ccc	768		
301	Tyr Gln Phe Leu Phe Pro Phe His Glu Asp Asn Glu Lys Asp Leu Pro			
302	165 170 175			
304	atc agt gaa aag ctc att gag gaa gat gca caa ttg acc caa atg gag	816		
305	Ile Ser Glu Lys Leu Ile Glu Glu Asp Ala Gln Leu Thr Gln Met Glu			
306	180 185 190			
308	gat gtg ttc agc cag ttg act gtg gat gtg aat tct ctc ttt aac agg	864		
309	Asp Val Phe Ser Gln Leu Thr Val Asp Val Asn Ser Leu Phe Asn Arg			
310	195 200 205			
312	agt ttt aac gtc ttc aga cag atg cag caa gag ttt gac cag act ttt	912		
313	Ser Phe Asn Val Phe Arg Gln Met Gln Gln Glu Phe Asp Gln Thr Phe			
314	210 215 220			
316	caa tca cat ttc ata tca gat aca gac cta act gag cct tac ttt ttt	960		
317	Gln Ser His Phe Ile Ser Asp Thr Asp Leu Thr Glu Pro Tyr Phe Phe			
318	225 230 235 240			
320	cca gct ttc tct aaa gag ccg atg aca aaa gca gat ctt gag caa tgt	1008		
321	Pro Ala Phe Ser Lys Glu Pro Met Thr Lys Ala Asp Leu Glu Gln Cys			
322	245 250 255			
324	tgg gac att ccc aac ttc ttc cag ctg ttt tgt aat ttc agt gtc tct	1056		
325	Trp Asp Ile Pro Asn Phe Phe Gln Leu Phe Cys Asn Phe Ser Val Ser			
326	260 265 270			
328	att tat gaa agt gtc agt gaa aca att act aag atg ctg aag gca ata	1104		
329	Ile Tyr Glu Ser Val Ser Glu Thr Ile Thr Lys Met Leu Lys Ala Ile			
330	275 280 285			
332	gaa gat tta cca aaa caa gac aaa gct cct gac cac gga ggc ctg att	1152		
333	Glu Asp Leu Pro Lys Gln Asp Lys Ala Pro Asp His Gly Gly Leu Ile			
334	290 295 300			
336	tca aag atg tta cct ggg cag gac aga gga ctg tgt ggg gaa ctt gac	1200		
337	Ser Lys Met Leu Pro Gly Gln Asp Arg Gly Leu Cys Gly Glu Leu Asp			
338	305 310 315 320			

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```

340 cag aat ttg tca aga tgt ttc aaa ttt cat gaa aaa tgc caa aaa tgt      1248
341 Gln Asn Leu Ser Arg Cys Phe Lys Phe His Glu Lys Cys Gln Lys Cys
342                               325                               330                               335
344 cag gct cac cta tct gaa gac tgt cct gat gta cct gct ctg cac aca      1296
345 Gln Ala His Leu Ser Glu Asp Cys Pro Asp Val Pro Ala Leu His Thr
346                               340                               345                               350
348 gaa tta gac gag gcg atc agg ttg gtc aat gta tcc aat cag cag tat      1344
349 Glu Leu Asp Glu Ala Ile Arg Leu Val Asn Val Ser Asn Gln Gln Tyr
350                               355                               360                               365
352 ggc cag att ctc cag atg acc cgg aag cac ttg gag gac acc gcc tat      1392
353 Gly Gln Ile Leu Gln Met Thr Arg Lys His Leu Glu Asp Thr Ala Tyr
354                               370                               375                               380
356 ctg gtg gag aag atg aga ggg caa ttt ggc tgg gtg tct gaa ctg gca      1440
357 Leu Val Glu Lys Met Arg Gly Gln Phe Gly Trp Val Ser Glu Leu Ala
358 385                               390                               395                               400
360 aac cag gcc cca gaa aca gag atc atc ttt aat tca ata cag gta gtt      1488
361 Asn Gln Ala Pro Glu Thr Glu Ile Ile Phe Asn Ser Ile Gln Val Val
362                               405                               410                               415
364 cca agg att cat gaa gga aat att tcc aaa caa gat gaa aca atg atg      1536
365 Pro Arg Ile His Glu Gly Asn Ile Ser Lys Gln Asp Glu Thr Met Met
366                               420                               425                               430
368 aca gac tta agc att ctg cct tcc tct aat ttc aca ctc aag atc cct      1584
369 Thr Asp Leu Ser Ile Leu Pro Ser Ser Asn Phe Thr Leu Lys Ile Pro
370                               435                               440                               445
372 ctt gaa gaa agt gct gag agt tct aac ttc att ggc tac gta gtg gca      1632
373 Leu Glu Glu Ser Ala Glu Ser Ser Asn Phe Ile Gly Tyr Val Val Ala
374                               450                               455                               460
376 aaa gct cta cag cat ttt aag gaa cat ttt aaa acc tgg taagaagatc      1681
377 Lys Ala Leu Gln His Phe Lys Glu His Phe Lys Thr Trp
378 465                               470                               475
380 taatgcatcc tataatccagt aagtagaatt atctcttcat ctgggacctg gaaatcctga      1741
381 aataaaaaaag gataatgcaa taaacacagt tgcaggaaaag tatgttagct atatactatg      1801
382 aagtactctt agtttactta tgttgaatgg cttagctatt aataactcaaa ttgagttaaa      1861
383 atgaaaattc ctcttaaaaa aatcaaactg aatatgtatt acatttcatg gtacattagt      1921
384 agttctttgt atattgaata aataactaaat caccta                                1957

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/722,544A

DATE: 03/18/2002

TIME: 15:28:24

Input Set : A:\07334-362001.txt

Output Set: N:\CRF3\03182002\I722544A.raw

L:255 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:3 differs:1
L:776 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:777 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:1028 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:1030 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:1031 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:1032 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:1228 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:1229 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:1407 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:1455 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:1477 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:1517 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:1518 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:1519 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:1735 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:1736 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:1737 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:1738 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7